SEQUENCE LISTING

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<110> REPKE, HEINRICH
     BUDDE, ECKHARD
     NICOLAUS, STEFAN
<120> PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
     BEING IMMOBILIZED
<130> ALBRE-22
<140> 10/059,271
<141> 2002-01-31
<150> DE 101 06 295
<151> 2001-02-02
<160> 97
<170> PatentIn Ver. 2.1
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 Cys Ala Phe Arg Gln Val Cys His
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Ala Thr
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 Ile Arg Gln Gly Ile His Ile Gly Pro Gly Arg Ala Phe Phe Ala Ala
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Ala Thr Cys Thr
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Lys Ile Glu
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Asn Val
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 <210> 32
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 Thr Gly
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<210> 37
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Ala Val Gly Ile Gly Ile Asn Cys Thr Arg Pro Asn Asn Asn
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<210> 38
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Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Gly Pro
Thr Pro Thr
<210> 39
<211> 19
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Gly Lys Arg Ala His Lys Ser Arg Lys His Asn Tyr Lys Arg His Ile
Arg Arg Gly
<210> 40
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Gly Ser Lys Lys Ala Arg Arg Ile Lys Gly Lys Met Arg Arg Leu Lys
Lys Val Gly
<210> 41
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<400> 41
Gly Val Cys Ile Lys His Arg Tyr Lys Arg Lys Asp Lys Arg Lys His
Lys Val Ala Cys Ile Gly
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<210> 42
<211> 37
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<223> Description of Artificial Sequence: Synthetic
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<400> 42
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atatggcata tgtttttaga tggaatagat aaggccc
<210> 43
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<400> 43
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tatagggccc aggtggcagg ttaaaa
<210> 44
<211> 37
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atatggcata tgtttttaga tggaatagat aaggccc
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Met Phe Leu Asp Gly Ile Asp Lys Ala Gln Asp Glu His Glu Lys Tyr
His Ser Asn Trp Arg
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<210> 47
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Ala Met Ala Ser Asp Phe Asn Leu Pro Pro
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Ala Met Ala Ser Asp Phe Asn Leu Pro Pro
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tatagggccc aggtggcagg ttaaaa
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Lys Ala Gly
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taatttgccg gcgtagtagc aaaagaaata gtag
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Leu Lys Gly Glu Ala Met
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His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr
                   5
  1
                                                                    60
cat tta gaa gga
His Leu Glu Gly
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 <210> 61
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 His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr
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 His Leu Glu Gly
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Lys Val Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu Ala
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gaa gtt att cca
Glu Val Ile Pro
<210> 63
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<213> Artificial Sequence

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                                      10
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ctaggcaggc cactttatgc ttccgacgat cgcgtcgctt gtagcggtgt ttgatg
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 attatectag gteaaatgge agtatteate cae
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       oligonucleotide
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 tataggatec taatecteat cetgtetaet tge
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      oligonucleotide
<400> 74
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attatectag gteaaatgge agtatteate cae
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ggggaaagaa tagtagacat aatagcaaca gacatacaaa ctaaagaatt acaaaaacaa 120
attacaaaaa ttcaaaattt tcgggtttat tacagggaca gcagaaatcc actttggaaa 180
ggaccagcaa ageteetetg gaaaggtgaa ggggcagtag taatacaaga taatagtgac 240
ataaaagtag tgccaagaag aaaagcaaag atcattaggg attatggaaa acagatggca 300
ggtgatgatt gtgtggcaag tagacaggat gaggattag
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 Gly Ile Gly Gly Tyr Ser Ala Gly Glu Arg Ile Val Asp Ile Ile Ala
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 Thr Asp Ile Gln Thr Lys Glu Leu Gln Lys Gln Ile Thr Lys Ile Gln
  Asn Phe Arg Val Tyr Tyr Arg Asp Ser Arg Asn Pro Leu Trp Lys Gly
                           55
  Pro Ala Lys Leu Leu Trp Lys Gly Glu Gly Ala Val Val Ile Gln Asp
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  Asn Ser Asp Ile Lys Val Val Pro Arg Arg Lys Ala Lys Ile Ile Arg
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  Asp Tyr Gly Lys Gln Met Ala Gly Asp Asp Cys Val Ala Ser Arg Gln
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Asp Glu Asp
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aagggcaaaa tgcgacgggt gaagaaagcc ggcgtagtag caaaagaaat agtagccagc 180
tgtgataaat gtcagctaaa aggagaagcc atgcatggac aagtagactg tagtccagga 240
atatggcaac tagattgtac acatttagaa ggaaaagtta teetggtage agttcatgta 300
gccagtggat atatagaagc agaagttatt ccagcagaaa cagggcagga aacagcatat 360
ggagcatgca tcaaacaccg ctacaagcga cgcgatcgtc ggaagcataa agtggcctgc 420
ctaggtcaaa tggcagtatt catccacaat tttaaaaagaa aaggggggat tggggggtac 480
agtgcagggg aaagaatagt agacataata gcaacagaca tacaaactaa agaattacaa 540
aaacaaatta caaaaattca aaattttcgg gtttattaca gggacagcag aaatccactt 600
tggaaaggac cagcaaagct cctctggaaa ggtgaagggg cagtagtaat acaagataat 660
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 <211> 253
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 <213> Artificial Sequence
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 Met Phe Leu Asp Gly Ile Asp Lys Ala Gln Asp Glu His Glu Lys Tyr
 His Ser Asn Trp Arg Ala Met Ala Ser Asp Phe Asn Leu Pro Pro Gly
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25

20

Pro Lys Lys Ala Arg Arg Ile Lys Gly Lys Met Arg Arg Val Lys Lys
35 40 45

Ala Gly Val Val Ala Lys Glu Ile Val Ala Ser Cys Asp Lys Cys Gln 50 55 60

Leu Lys Gly Glu Ala Met His Gly Gln Val Asp Cys Ser Pro Gly Ile 65 70 75 80

Trp Gln Leu Asp Cys Thr His Leu Glu Gly Lys Val Ile Leu Val Ala 85 90 95

Val His Val Ala Ser Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu 100 105 110

Thr Gly Gln Glu Thr Ala Tyr Gly Ala Cys Ile Lys His Arg Tyr Lys 115 120 125

Arg Arg Asp Arg Lys His Lys Val Ala Cys Ile Gly Gln Met Ala 130 135 140

Val Phe Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser 145 150 155 160

Ala Gly Glu Arg Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys
165 170 175

Glu Leu Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr 180 185 190

Arg Asp Ser Arg Asn Pro Leu Trp Lys Gly Pro Ala Lys Leu Leu Trp 195 200 205

Lys Gly Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val 210 215 220

Val Pro Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met 225 230 235 240

Ala Gly Asp Asp Cys Val Ala Ser Arg Gln Asp Glu Asp 245 250

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<213> Artificial Sequence

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<400> 80

His His His His His

- <210> 81
- <211> 232
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- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence: Synthetic peptide
- <400> 81
- Met Gly Ser Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
- Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys
- Arg Arg Val Val Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ser Arg
- Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala
- Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys
- Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln
- Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr
- Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile
- Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr 135
- Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Glu 150 145
- Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp 170
- Asn Trp Phe Asn Ile Thr Asn Trp Leu Ala Met Glu Lys Tyr Leu Lys
- Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys 200
- His Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg
- Asp Arg Ser Ile Arg Leu Val Asn 230 225
- <210> 82
- <211> 254

- <212> PRT
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- <220>
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- <400> 82
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- Asn Leu Trp Gly Cys Lys Gly Arg Leu Val Cys Tyr Thr Asn Trp Arg
- Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
 35 40 45
- Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala
 50 55 60
- Val Gly Ile Gly Ser Arg Gln Leu Leu Ser Gly Ile Val Gln Gln 65 70 75 80
- Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu 85 90 95
- Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu 100 105 110
- Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
 115 120 125
- Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn 130 135 140
- Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp 145 150 155 160
- Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu
 165 170 175
- Ser Gln Asn Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp 180 185 190
- Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Ala 195 200 205
- Met Glu Lys Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys 210 215 220
- Ala Phe Arg Gln Val Cys His Asp Arg Pro Glu Gly Ile Glu Glu 225 230 235 240
- Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn 245 250

- <210> 83
- <211> 297
- <212> PRT
- <213> Artificial Sequence
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- Arg Gly Ala Val Gly Ile Gly Ile Asn Cys Thr Arg Pro Asn Asn Asn 20 25 30
- Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr 35 40 45
- Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Gly Pro 50 55 60
- Thr Pro Thr Gly Trp Lys Lys Asn Arg Arg Leu Lys Gly Lys Tyr Arg 65 70 75 80
- Arg Met Lys Lys Trp Gly Ala Val Gly Ile Gly Ile Asn Cys Thr Arg
- Pro Asn Asn His Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg
- Ala Phe Tyr Ala Thr Ser Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala 115 120 125
- His Cys Asn Ile Gly Pro Thr Pro Thr Gly Ala Cys Val Lys His Arg 130 135 140
- Gln Lys Arg Lys Glu Lys Arg Lys Tyr Lys Thr Ala Cys Val Gly Ala 145 150 155 160
- Val Gly Ile Gly Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 165 170 175
- Ser Ile His Leu Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Asp Gly 180 185 190
- Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Gly Pro Thr 195 200 205
- Pro Thr Gly Ser Lys Lys Ala Arg Arg Ile Lys Gly Lys Met Arg Arg 210 215 220
- Leu Lys Lys Val Gly Ala Val Gly Ile Gly Ile Asn Cys Thr Arg Pro 225 230 235 240
- Asn Asn Asn Gly His Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln
 245 250 255

Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His 260 265 270

Cys Asn Ile Gly Pro Thr Pro Thr Gly Lys Arg Ala Val Lys Ser Arg 275 280 285

Lys Tyr Lys Arg His Ile Arg Arg Gly

<210> 84

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<212> PRT

<213> Artificial Sequence

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Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys 20 25 30

Arg Arg Val Val Gln Arg Glu Ala Leu Glu Thr Leu Leu Gln Asn Gln
35 40 45

Gln Ile Leu Asn Leu Trp Gly Cys Lys Gly Arg Leu Ile Cys Tyr Trp
50 55 60

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu 65 70 75 80

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu 100 105 110

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile 115 120 125

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn 130 140

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala 145 150 155 160

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Ala Ile Glu Lys 165 170 175

Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg

Gln Val Cys His Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Glu 195 200 205

Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser 210 215 220

<210> 85

<211> 500

<212> PRT

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His 130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala 210 215 220 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu 290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser 355 360 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg 370 375 380

Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys 405 410 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn 420 425 430

Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe 435 440 445

Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg 450 455 460

Ser Gly Val Glu Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp 465 470 475 480

Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp 485 490 495

Pro Ser Ser Gln 500

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
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His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
     50
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
                 85
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
         115
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Ser Gln Asn Tyr Gly Lys Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg

135

- Xaa Xaa Arg Arg Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg 145 150 155 160
- Xaa Arg Arg Lys Xaa Lys Xaa Cys Xaa Gly Pro Ile Val Gln Asn 165 170 175
- Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn 180 185 190
- Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile 195 200 205
- Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn 210 215 220
- Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu 225 230 235 240
- Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro 245 250 255
- Val His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly 260 265 270
- Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp 275 280 285
- Gly Xaa Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys 290 295 300
- Lys Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg 305 310 315 320
- Arg Lys Xaa Lys Xaa Cys Xaa Gly Met Thr Asn Asn Pro Pro Ile
- Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys 340 345 350
- Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly 355 360 365
- Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu 370 375 380
- Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr 385 390 395 400
- Leu Leu Val Gly Lys Arg Xaa Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa 405 410 415
- Xaa Arg Arg Gly Gly Xaa Lys Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa
 420 425 430
- Arg Arg Xaa Lys Lys Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys 435 440 445

Arg Arg Xaa Arg Arg Lys Xaa Lys Xaa Xaa Cys Xaa Gly Gln Asn Ala

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr 465 470 475 480

Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His
485 490 495

Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr Asn Ser Ala 500 505 510

Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg Lys Ile Val 515 520 525

Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr Ala Arg Asn Cys Arg 530 535 540

Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly His Gln 545 550 555 560

Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys Ile Trp 565 570 575

Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe Leu Gln Gly Lys Arg Xaa 580 585 590

Xaa Lys Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa Lys 595 600 605

Lys Xaa Arg Arg Xaa Lys Gly Lys Xaa Arg Arg Xaa Lys Lys Xaa Gly 610 615 620

Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa Arg Arg Lys Xaa 625 630 635 640

Lys Xaa Xaa Cys Xaa Gly Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu 655

Glu Ser Phe Arg Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln 660 665 670

Glu Pro Ile Asp Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu 675 680 685

Phe Gly Asn Asp Pro Ser Ser Gln 690 695

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<211> 561

<212> PRT

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Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile
35 40 45

Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile 50 55 60

Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu 65 70 75 80

Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro 85 90 95

His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val

Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr 115 120 125

Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg 130 135 140

Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile 145 150 155 160

Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn 165 170 175

Pro Asn Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser 180 185 190

Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln 195 200 205

His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys 210 215 220

Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp 225 230 235 240

Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn 245 250 255

Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr 260 265 270

Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys 275 280 285

Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu 290 295 300

Ala	Glu	Asn	Arq	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr
305			_		310		-			315					320

- Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly 325 330 335
- Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr 340 345 350
- Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln 355 360 365
- Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp 370 375 380
- Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu
- Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu
 405 410 415
- Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys 420 425 430
- Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn 435 440 445
- Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly Arg 450 455 460
- Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu Leu 465 470 475 480
- Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn Ile 485 490 495
- Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp 500 505 510
- Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile Lys 515 520 525
- Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile Gly 530 535 540
- Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys Val 545 550 555 560

Leu

<210> 88

<211> 851

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Arg Lys Xaa Lys Xaa Xaa Cys Xaa Gly Val Val Ala Lys Glu Ile Val

Ala Ser Cys Asp Lys Cys Gln Leu Lys Gly Glu Ala Met His Gly Gln

Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr His Leu Glu

Gly Lys Val Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu

Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr Gly Lys 145

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- Lys Xaa Lys Xaa Cys Xaa Gly Phe Leu Leu Lys Leu Ala Gly Arg 210 215 220
- Trp Pro Val Lys Thr Ile His Thr Asp Asn Gly Ser Asn Phe Thr Ser 225 230 235 240
- Ala Thr Val Lys Ala Ala Cys Trp Trp Ala Gly Ile Lys Gln Glu Phe
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- Lys Lys Xaa Gly Gly Xaa Cys Xaa Lys Xaa Arg Xaa Lys Arg Arg Xaa 290 295 300
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- Gln Ser Gln Gly Val Val Glu Ser Met Asn Lys Glu Leu Lys Lys Ile 325 330 335
- Ile Gly Gln Val Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gly 340 345 350
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- Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys Glu Leu Gln Lys
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35 40 45

Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val Val Leu Val Asn 50 55 60

Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met Val Glu Gln Met 65 70 75 80

His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val 85 90 95

Lys Leu Thr Pro Leu Cys Val Ser Leu Lys Glu Cys Thr Asp Leu Lys
100 105 110

Asn Asp Thr Asn Thr Asn Ser Ser Ser Gly Arg Met Ile Met Glu Lys 115 120 125

Gly Glu Ile Lys Asn Cys Ser Asn Ile Ser Thr Ser Ile Arg Gly Lys
130 135 140

Val Gln Lys Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile 145 150 155 160

Asp Asn Asp Thr Thr Ser Tyr Lys Leu Thr Ser Cys Asn Thr Ser Val

Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His 180 185 190

- Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr 195 200 205
- Phe Asn Gly Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr 210 215 220
- His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser 225 230 235 240
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Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser 130 135 140

Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met 145 150 155 160

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- Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg 165 170 175
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- Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro 210 215 220
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- Xaa Arg Lys Xaa Lys Arg Xaa Xaa Arg Arg Gly Gly Xaa Lys Lys Xaa
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- Xaa Arg Arg Lys Xaa Lys Xaa Cys Xaa Gly Ile Ala Tyr Ile His
- Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Arg Leu Tyr Ser Ile 435 440 445
- Cys Arg Asp Leu Leu Ser Arg Ser Phe Leu Thr Leu Gln Leu Ile Tyr 450 455 460
- Gln Asn Leu Arg Asp Trp Leu Arg Leu Arg Thr Ala Phe Leu Gln Tyr 465 470 475 480
- Gly Cys Glu Trp Ile Gln Glu Ala Phe Gln Ala Ala Ala Arg Ala Thr 485 490 495
- Arg Glu Thr Leu Ala Gly Ala Cys Arg Gly Leu Trp Arg Val Leu Glu 500 505 510
- Arg Ile Gly Arg Gly Ile Leu Ala Val Pro Arg Arg Ile Arg Gln Gly 515 520 525
- Ala Glu Ile Ala Leu Leu 530
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- <212> PRT
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence: Synthetic
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Asn Leu Trp Gly Cys Lys Gly Arg Leu Val Cys Tyr Thr Asn Trp Arg 20 25 30

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val 35 40 45

Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala 50 60

Val Gly Ile Gly Ser Arg Gln Leu Leu Ser Gly Ile Val Gln Gln 65 70 75 80

Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu 85 90 95

Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu 100 105 110

Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
115 120 125

Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn 130 135 140

Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp 145 150 155 160

Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu 165 170 175

Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp 180 185 190

Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Ala 195 200 205

Met Glu Lys Tyr Leu Lys Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys 210 215 220

Ala Phe Arg Gln Val Cys His Asp Arg Pro Glu Gly Ile Glu Glu 225 230 235 240

Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser 245 250 255